

SEQUENCE LISTING

5 SEQ ID NO: 1 is a primate IL-B30 natural nucleic acid sequence.
SEQ ID NO: 2 is a primate IL-B30 natural amino acid sequence.
SEQ ID NO: 3 is a rodent IL-B30 natural nucleic acid sequence.
SEQ ID NO: 4 is a rodent IL-B30 natural amino acid sequence.
SEQ ID NO: 5 is a pig IL-B30.
10 SEQ ID NO: 6 is bovine G-CSF.
SEQ ID NO: 7 is feline G-CSF.
SEQ ID NO: 8 is human G-CSF.
SEQ ID NO: 9 is mouse G-CSF.
SEQ ID NO: 10 is otter IL-6.
15 SEQ ID NO: 11 is feline IL-6.
SEQ ID NO: 12 is human IL-6.
SEQ ID NO: 13 is sheep IL-6.
SEQ ID NO: 14 is mouse IL-6.
SEQ ID NO: 15 is chicken MGF.
20 SEQ ID NO: 16 is KSHV, kaposi's sarcoma herpes virus, a viral IL-6.

(1) GENERAL INFORMATION:

25 (i) APPLICANT: Bazan, J. Fernando.

(ii) TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

30 (A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
(D) STATE: California
35 (E) COUNTRY: USA
(F) ZIP: 94304-1104

(v) COMPUTER READABLE FORM:

40 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

45 (A) APPLICATION NUMBER: US
(B) FILING DATE: 24-JUL-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

50 (A) APPLICATION NUMBER: US 60/053,765
(B) FILING DATE: 25-JUL-1997

(viii) ATTORNEY/AGENT INFORMATION:

55 (A) NAME: Ching, Edwin P.
(B) REGISTRATION NUMBER: 34,090
(C) REFERENCE/DOCKET NUMBER: DX0758K1

(ix) TELECOMMUNICATION INFORMATION:

60 (A) TELEPHONE: (650)852-9196
(B) TELEFAX: (650)496-1200

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 570 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..567

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 64..567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

25	ATG CTG GGG AGC AGA GCT GTA ATG CTG CTG TTG CTG CTG CCC TGG ACA	48
	Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Leu Pro Trp Thr	
	-21 -20 -15 -10	
30	GCT CAG GGC AGA GCT GTG CCT GGG GGC AGC AGC CCT GCC TGG ACT CAG	96
	Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln	
	-5 1 5 10	
35	TGC CAG CAG CTT TCA CAG AAG CTC TGC ACA CTG GCC TGG AGT GCA CAT	144
	Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His	
	15 20 25	
40	CCA CTA GTG GGA CAC ATG GAT CTA AGA GAA GAG GGA GAT GAA GAG ACT	192
	Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr	
	30 35 40	
45	ACA AAT GAT GTT CCC CAT ATC CAG TGT GGA GAT GGC TGT GAC CCC CAA	240
	Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln	
	45 50 55	
50	GGA CTC AGG GAC AAC AGT CAG TTC TGC TTG CAA AGG ATC CAC CAG GGT	288
	Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly	
	60 65 70 75	
55	CTG ATT TTT TAT GAG AAG CTG CTA GGA TCG GAT ATT TTC ACA GGG GAG	336
	Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu	
	80 85 90	
60	CCT TCT CTG CTC CCT GAT AGC CCT GTG GCG CAG CTT CAT GCC TCC CTA	384
	Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu	
	95 100 105	
65	CTG GGC CTC AGC CAA CTC CTG CAG CCT GAG GGT CAC CAC TGG GAG ACT	432
	Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr	
	110 115 120	

005240"42485560

CAG CAG ATT CCA AGC CTC AGT CCC AGC CAG CCA TGG CAG CGT CTC CTT 480
 Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu
 125 130 135

5 CTC CGC TTC AAA ATC CTT CGC AGC CTC CAG GCC TTT GTG GCT GTA GCC 528
 Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala
 140 145 150 155

10 GCC CGG GTC TTT GCC CAT GGA GCA GCA ACC CTG AGT CCC TAA 570
 Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro
 160 165

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Leu Pro Trp Thr
 -21 -20 -15 -10

Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln
 -5 1 5 10

30 Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His
 15 20 25

35 Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr
 30 35 40

Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln
 45 50 55

40 Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly
 60 65 70 75

Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu
 80 85 90

45 Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu
 95 100 105

50 Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr
 110 115 120

Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu
 125 130 135

55 Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala
 140 145 150 155

Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro
 160 165

60

005240-12485560

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 113..700

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 176..700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

CGCTTAGAAG TCGGACTACA GAGTTAGACT CAGAACCAAA GGAGGTGGAT AGGGGGTCCA      60
CAGGCCTGGT GCAGATCACA GAGCCAGCCA GATCTGAGAA GCAGGGAACA AG ATG      115
                                     Met
                                     -21

CTG GAT TGC AGA GCA GTA ATA ATG CTA TGG CTG TTG CCC TGG GTC ACT      163
Leu Asp Cys Arg Ala Val Ile Met Leu Trp Leu Leu Pro Trp Val Thr
-20                               -15                               -10                               -5

CAG GGC CTG GCT GTG CCT AGG AGT AGC AGT CCT GAC TGG GCT CAG TGC      211
Gln Gly Leu Ala Val Pro Arg Ser Ser Ser Pro Asp Trp Ala Gln Cys
                               1                               5                               10

CAG CAG CTC TCT CGG AAT CTC TGC ATG CTA GCC TGG AAC GCA CAT GCA      259
Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His Ala
                               15                               20                               25

CCA GCG GGA CAT ATG AAT CTA CTA AGA GAA GAA GAG GAT GAA GAG ACT      307
Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu Thr
                               30                               35                               40

AAA AAT AAT GTG CCC CGT ATC CAG TGT GAA GAT GGT TGT GAC CCA CAA      355
Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro Gln
                               45                               50                               55                               60

GGA CTC AAG GAC AAC AGC CAG TTC TGC TTG CAA AGG ATC CGC CAA GGT      403
Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln Gly
                               65                               70                               75

CTG GCT TTT TAT AAG CAC CTG CTT GAC TCT GAC ATC TTC AAA GGG GAG      451
Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly Glu
                               80                               85                               90

CCT GCT CTA CTC CCT GAT AGC CCC ATG GAG CAA CTT CAC ACC TCC CTA      499
Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser Leu
                               95                               100                               105

```

005240" 4248560

CTA GGA CTC AGC CAA CTC CTC CAG CCA GAG GAT CAC CCC CGG GAG ACC 547
 Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu Thr
 110 115 120

5 CAA CAG ATG CCC AGC CTG AGT TCT AGT CAG CAG TGG CAG CGC CCC CTT 595
 Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro Leu
 125 130 135 140

10 CTC CGT TCC AAG ATC CTT CGA AGC CTC CAG GCC TTT TTG GCC ATA GCT 643
 Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile Ala
 145 150 155

15 GCC CGG GTC TTT GCC CAC GGA GCA GCA ACT CTG ACT GAG CCC TTA GTG 691
 Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu Val
 160 165 170

CCA ACA GCT TAAGGATGCC CAGGTTCCCA TGGCTACCAT GATAAGACTA 740
 Pro Thr Ala
 175

20 ATCTATCAGC CCAGACATCT ACCAGTTAAT TAACCCATTA GGACTTGTGC TGTTCTTGTT 800

TCGTTTGTTT TGCCTGAAGG GCAAGGACAC CATTATTAAA GAGAAAAGAA ACAAACCCCA 860

25 GAGCAGGCAG CTGGCTAGAG AAAGGAGCTG GAGAAGAAGA ATAAAGTCTC GAGCCCTTGG 920

CCTTGGAAGC GGGCAAGCAG CTGCGTGGCC TGAGGGGAAG GGGCGGTGG CATCGAGAAA 980

30 CTGTGAGAAA ACCCAGAGCA TCAGAAAAAG TGAGCCCAGG CTTTGGCCAT TATCTGTAAG 1040

AAAAACAAGA AAAGGGGAAC ATTATACTTT CCTGGGTGGC TCAGGGAAAT GTGCAGATGC 1100

ACAGTACTCC AGACAGCAGC TCTGTACCTG CCTGCTCTGT CCCTCAGTTC TAACAGAATC 1160

35 TAGTCACTAA GAACTAACAG GACTACCAAT ACGAACTGAC AAA 1203

(2) INFORMATION FOR SEQ ID NO:4:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

50 Met Leu Asp Cys Arg Ala Val Ile Met Leu Trp Leu Leu Pro Trp Val
 -21 -20 -15 -10

Thr Gln Gly Leu Ala Val Pro Arg Ser Ser Ser Pro Asp Trp Ala Gln
 -5 1 5 10

55 Cys Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His
 15 20 25

Ala Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu
 30 35 40

60

005240-42485560

Thr Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro
 45 50 55
 5 Gln Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln
 60 65 70 75
 Gly Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly
 80 85 90
 10 Glu Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser
 95 100 105
 Leu Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu
 110 115 120
 15 Thr Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro
 125 130 135
 20 Leu Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile
 140 145 150 155
 Ala Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu
 160 165 170
 25 Val Pro Thr Ala
 175
 (2) INFORMATION FOR SEQ ID NO:5:
 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: peptide
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
 Ser Cys Leu Gln Arg Ile His Gln Gly Leu Val Phe Tyr Glu Lys Leu
 1 5 10 15
 45 Leu Gly Ser Asp Ile Phe Thr Gly Glu Pro Ser Leu His Pro Asp Gly
 20 25 30
 Ser Val Gly Gln Leu His Ala Ser Leu Leu Gly Leu Arg Gln Leu Leu
 35 40 45
 50 Gln Pro Glu Gly His His Trp Glu Thr Glu Gln Thr Pro Ser Pro Ser
 50 55 60
 55 Pro Ser Gln Pro Trp Gln Arg Leu Leu Leu Arg Leu Lys Ile Leu Arg
 65 70 75 80
 Ser Leu Gln Ala Phe Val Ala Val Ala Ala Arg Val Phe Ala His Gly
 85 90 95
 60

005240-42485560

Ala Ala Thr Leu Ser Gln
100

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr Pro Leu Gly Pro Ala Arg Ser Leu Pro Gln Ser Phe Leu Leu Lys
1 5 10 15
Cys Leu Glu Gln Val Arg Lys Ile Gln Ala Asp Gly Ala Glu Leu Gln
20 25 30
Glu Arg Leu Cys Ala Ala His Lys Leu Cys His Pro Glu Glu Leu Met
35 40 45
Leu Leu Arg His Ser Leu Gly Ile Pro Gln Ala Pro Leu Ser Ser Cys
50 55 60
Ser Ser Gln Ser Leu Gln Leu Arg Gly Cys Leu Asn Gln Leu His Gly
65 70 75 80
Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Ala Gly Ile Ser
85 90 95
Pro Glu Leu Ala Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Thr Asp
100 105 110
Phe Ala Thr Asn Ile Trp Leu Gln Met Glu Asp Leu Gly Ala Ala Pro
115 120 125
Ala Val Gln Pro Thr Gln Gly Ala Met Pro Thr Phe Thr Ser Ala Phe
130 135 140
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser Gln Leu His Arg Phe
145 150 155 160
Leu Glu Leu Ala Tyr Arg Gly Leu Arg Tyr Leu Ala Glu Pro
165 170

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Thr Pro Leu Gly Pro Thr Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1 5 10 15

Cys Leu Glu Gln Val Arg Lys Val Gln Ala Asp Gly Thr Ala Leu Gln
20 25 30

Glu Arg Leu Cys Ala Ala His Lys Leu Cys His Pro Glu Glu Leu Val
35 40 45

Leu Leu Gly His Ala Leu Gly Ile Pro Gln Ala Pro Leu Ser Ser Cys
50 55 60

Ser Ser Gln Ala Leu Gln Leu Thr Gly Cys Leu Arg Gln Leu His Ser
65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Ala Gly Ile Ser
85 90 95

Pro Glu Leu Ala Pro Thr Leu Asp Met Leu Gln Leu Asp Ile Thr Asp
100 105 110

Phe Ala Ile Asn Ile Trp Gln Gln Met Glu Asp Val Gly Met Ala Pro
115 120 125

Ala Val Pro Pro Thr Gln Gly Thr Met Pro Thr Phe Thr Ser Ala Phe
130 135 140

Gln Arg Arg Ala Gly Gly Thr Leu Val Ala Ser Asn Leu Gln Ser Phe
145 150 155 160

Leu Glu Val Ala Tyr Arg Ala Leu Arg His Phe Thr Lys Pro
165 170

40 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
(B) TYPE: amino acid
45 (C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1 5 10 15

Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
20 25 30

005240-12185560

Glu Lys Leu Val Ser Glu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu
35 40 45

Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
50 55 60

Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln
65 70 75 80

Leu His Ser Gly Leu Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala
85 90 95

Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu
100 105 110

Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu
115 120 125

Arg His Leu Ala Gln Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
130 135 140

Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
145 150 155 160

Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly
165 170 175

Pro

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Pro Leu Val Thr Val Ser Ala Leu Pro Pro Ser Leu Pro Leu Pro
1 5 10 15

Arg Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Ala
20 25 30

Ser Gly Ser Val Leu Leu Glu Gln Leu Cys Ala Thr Tyr Lys Leu Cys
35 40 45

His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Lys
50 55 60

Ala Ser Leu Ser Gly Cys Ser Ser Gln Ala Leu Gln Gln Thr Gln Cys
65 70 75 80

005240-42485560

[illegible]

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

[illegible]

Thr Leu Arg Pro Met Asn Gln Ile Glu Val Thr Thr Pro Asp Pro Thr
130 135 140

5 Thr Asp Ala Ser Leu Gln Ala Leu Phe Lys Ser Gln Asp Lys Trp Leu
145 150 155 160

Lys His Thr Thr Ile His Leu Ile Leu Arg Arg Leu Glu Asp Phe Leu
165 170 175

10 Gln Phe Ser Leu Arg Ala Ile Arg Ile Met
180 185

(2) INFORMATION FOR SEQ ID NO:11:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30 Ala Phe Pro Thr Pro Gly Pro Leu Gly Gly Asp Ala Thr Ser Asn Arg
1 5 10 15

Leu Pro Leu Thr Pro Ala Asp Lys Met Glu Glu Leu Ile Lys Tyr Ile
20 25 30

35 Leu Gly Lys Ile Ser Ala Leu Lys Lys Glu Met Cys Asp Asn Tyr Asn
35 40 45

Lys Cys Glu Asp Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu
50 55 60

40 Pro Lys Leu Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Gln
65 70 75 80

Glu Thr Cys Leu Thr Arg Ile Thr Thr Gly Leu Gln Glu Phe Gln Ile
85 90 95

45 Tyr Leu Lys Phe Leu Gln Asp Lys Tyr Glu Gly Asp Lys Glu Asn Ala
100 105 110

50 Lys Ser Val Tyr Thr Ser Thr Asn Val Leu Leu Gln Met Leu Lys Arg
115 120 125

Lys Gly Lys Asn Gln Asp Glu Val Thr Ile Pro Val Pro Thr Val Glu
130 135 140

55 Val Gly Leu Gln Leu Ser Cys Ser His Arg Arg Val Ala Glu Ala His
145 150 155 160

Asn Asn His Leu Thr Leu Arg Arg Leu Glu Asp Phe Leu Gln Leu Arg
165 170 175

60

005240:42485560

Leu Arg Ala Val Arg Ile Met
180

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala Phe Pro Ala Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala
1 5 10 15

Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln
20 25 30

Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys
35 40 45

Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn
50 55 60

Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser
65 70 75 80

Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu
85 90 95

Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser
100 105 110

Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln
115 120 125

Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp
130 135 140

Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln
145 150 155 160

Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu
165 170 175

Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
180 185

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10 Ala Phe Pro Thr Pro Gly Pro Leu Gly Glu Asp Phe Lys Asn Asp Thr
1 5 10 15

Thr Pro Ser Arg Leu Leu Leu Thr Thr Pro Glu Lys Thr Glu Ala Leu
20 25 30

15 Ile Lys His Ile Val Asp Lys Ile Ser Ala Ile Arg Lys Glu Ile Cys
35 40 45

20 Glu Lys Asn Asp Glu Cys Glu Asn Ser Lys Glu Thr Leu Ala Glu Asn
50 55 60

Lys Leu Lys Leu Pro Lys Met Glu Glu Lys Asp Gly Cys Phe Gln Ser
65 70 75 80

25 Gly Phe Asn Gln Ala Ile Cys Leu Ile Lys Thr Thr Ala Gly Leu Leu
85 90 95

Glu Tyr Gln Ile Tyr Leu Asp Phe Leu Gln Asn Glu Phe Glu Gly Asn
100 105 110

30 Gln Glu Thr Val Met Glu Leu Gln Ser Ser Ile Arg Thr Leu Ile Gln
115 120 125

35 Ile Leu Lys Glu Lys Ile Ala Gly Leu Ile Thr Thr Pro Ala Thr His
130 135 140

Thr Asp Met Leu Glu Lys Met Gln Ser Ser Asn Glu Trp Val Lys Asn
145 150 155 160

40 Ala Lys Val Ile Ile Ile Leu Arg Ser Leu Glu Asn Phe Leu Gln Phe
165 170 175

Ser Leu Arg Ala Ile Arg Met Lys
180

45

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: peptide

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

60

005240"4248550

005240-42485560

	Ala	Phe	Pro	Thr	Ser	Gln	Val	Arg	Arg	Gly	Asp	Phe	Thr	Glu	Asp	Thr	
	1				5					10					15		
5	Thr	Pro	Asn	Arg	Pro	Val	Tyr	Thr	Thr	Ser	Gln	Val	Gly	Gly	Leu	Ile	
				20					25					30			
	Thr	His	Val	Leu	Trp	Glu	Ile	Val	Glu	Met	Arg	Lys	Glu	Leu	Cys	Asn	
			35					40					45				
10	Gly	Asn	Ser	Asp	Cys	Met	Asn	Asn	Asp	Asp	Ala	Leu	Ala	Glu	Asn	Asn	
		50					55					60					
	Leu	Lys	Leu	Pro	Glu	Ile	Gln	Arg	Asn	Asp	Gly	Cys	Tyr	Gln	Thr	Gly	
15	65					70					75					80	
	Tyr	Asn	Gln	Glu	Ile	Cys	Leu	Leu	Lys	Ile	Ser	Ser	Gly	Leu	Leu	Glu	
					85					90					95		
20	Tyr	His	Ser	Tyr	Leu	Glu	Tyr	Met	Lys	Asn	Asn	Leu	Lys	Asp	Asn	Lys	
				100					105					110			
	Lys	Asp	Lys	Ala	Arg	Val	Leu	Gln	Arg	Asp	Thr	Glu	Thr	Leu	Ile	His	
			115					120					125				
25	Ile	Phe	Asn	Gln	Glu	Val	Lys	Asp	Leu	His	Lys	Ile	Val	Leu	Pro	Thr	
		130					135						140				
	Pro	Ile	Ser	Asn	Ala	Leu	Leu	Thr	Asp	Lys	Leu	Glu	Ser	Gln	Lys	Glu	
30	145					150					155					160	
	Trp	Leu	Arg	Thr	Lys	Thr	Ile	Gln	Phe	Ile	Leu	Lys	Ser	Leu	Glu	Glu	
					165					170					175		
35	Phe	Leu	Lys	Val	Thr	Leu	Arg	Ser	Thr	Arg	Gln	Thr					
				180					185								

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala	Pro	Leu	Ala	Glu	Leu	Ser	Gly	Asp	His	Asp	Phe	Gln	Leu	Phe	Leu	
1				5					10					15		
His	Lys	Asn	Leu	Glu	Phe	Thr	Arg	Lys	Ile	Arg	Gly	Asp	Val	Ala	Ala	
			20					25					30			
Leu	Gln	Arg	Ala	Val	Cys	Asp	Thr	Phe	Gln	Leu	Cys	Thr	Glu	Glu	Glu	
		35					40					45				

Leu Gln Leu Val Gln Pro Asp Pro His Leu Val Gln Ala Pro Leu Asp
 50 55 60
 5 Gln Cys His Lys Arg Gly Phe Gln Ala Glu Val Cys Phe Thr Gln Ile
 65 70 75 80
 Arg Ala Gly Leu His Ala Tyr His Asp Ser Leu Gly Ala Val Leu Arg
 85 90 95
 10 Leu Leu Pro Asn His Thr Thr Leu Val Glu Thr Leu Gln Leu Asp Ala
 100 105 110
 Ala Asn Leu Ser Ser Asn Ile Gln Gln Gln Met Glu Asp Leu Gly Leu
 115 120 125
 15 Asp Thr Val Thr Leu Pro Ala Glu Gln Arg Ser Pro Pro Pro Thr Phe
 130 135 140
 20 Ser Gly Pro Phe Gln Gln Gln Val Gly Gly Phe Phe Ile Leu Ala Asn
 145 150 155 160
 Phe Gln Arg Phe Leu Glu Thr Ala Tyr Arg Ala Leu Arg His Leu Ala
 165 170 175
 25 Arg Leu

(2) INFORMATION FOR SEQ ID NO:16:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys Asp Leu Leu
 1 5 10 15
 45 Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu Cys Phe Arg
 20 25 30
 50 Asp Leu Cys Tyr Arg Thr Gly Ile Cys Lys Gly Ile Leu Glu Pro Ala
 35 40 45
 Ala Ile Phe His Leu Lys Leu Pro Ala Ile Asn Asp Thr Asp His Cys
 50 55 60
 55 Gly Leu Ile Gly Phe Asn Glu Thr Ser Cys Leu Lys Lys Leu Ala Asp
 65 70 75 80
 Gly Phe Phe Glu Phe Glu Val Leu Phe Lys Phe Leu Thr Thr Glu Phe
 85 90 95
 60

0058474-042500

5 Gly Lys Ser Val Ile Asn Val Asp Val Met Glu Leu Leu Thr Lys Thr
100 105 110

Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys Leu Thr Lys Thr His
115 120 125

Tyr Ser Pro Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg Leu Gln Gly
130 135 140

10 Leu Lys Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val Leu Ser Ala
145 150 155 160

Met Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp Ser Ile Pro
165 170 175

15 Asp Val Thr Pro Asp Val His Asp Lys
180 185

005240-42485560